

#3

SEQUENCE LISTING

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Dumoutier, Laure  
Polikarpov, Igor



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TECH CENTER 1600/2900

<120> Crystal Structure of Interleukin-22

<130> LUD-5722 US

<140> 10/050,552

<141> 2002-01-18

<150> 60/317,937

<151> 2001-09-10

<150> 60/333,150

<151> 2001-11-27

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 178

<212> PRT

<213> homo sapiens

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1 5 10 15

Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His  
20 25 30

Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe  
35 40 45

Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu  
50 55 60

Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Val Leu Gly Cys

65

70

75

80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro  
                     85                    90                    95

Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu  
                     100                    105                    110

Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg  
                     115                    120                    125

Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn  
                     130                    135                    140

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu  
                     145                    150                    155                    160

Glu Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile  
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Arg Asn

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Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala  
                     20                    25                    30

Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln  
                     35                    40                    45

Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser  
50 55 60

Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
65 70 75 80

His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu  
85 90 95

Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln  
100 105 110

Pro Tyr Met Gln Glu Val Val Pro Phe Ile Ala Arg Ile Ser Asn Arg  
115 120 125

Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn  
130 135 140

Val Gln Lys Leu Lys Asp Thr Val Lys Lys Ile Gly Glu Ser Gly Glu  
145 150 155 160

Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn  
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Ala Cys Ile

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Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu  
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Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn

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25

30

Ala Leu Pro Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln  
 35 40 45

Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Ile Ala Lys Glu Ala Ser  
 50 55 60

Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
 65 70 75 80

Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu  
 85 90 95

Asn Phe Thr Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln  
 100 105 110

Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln  
 115 120 125

Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn  
 130 135 140

Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu  
 145 150 155 160

Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn  
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Ala Cys Val

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<213> artificial sequence

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<223> A conserved sequence between Region 2 in IL-22 and IL-10

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Phe Thr Leu Glu Glu Val Leu  
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<210> 5

<211> 4

<212> PRT

<213> artificial sequence

<220>

<223> A conserved sequence between Region 2 of IL-22 and IL-10

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Lys Leu Gly Glu  
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10/050,552

-- CProject --

CProjectData #Crystal Structure of Interleukin-22  
LUD-5722-US

\_\_\_\_\_  
-- CProtein1Sequence SEQ ID NO: 1 h IL-1

homo  
sapiensYMHSSALLCCIVILTGVRASPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFQMKDQLDNLLLKESLLE  
DFKGVLCQALSEMIQFYLEEVMQAENQDPDIKAHVNSLGENLKTLLRLRLRRCHRLFPCENKSKAVEQVKNAFNKLQEK  
GIYKAMSEEDIFINYIEAYMTMKIRN ARNDBCQEZHILKMFPSTWYVX PRT  
-- CCommentFeature EU; e SEQ ID NO:2 hu IL-2

(portion of submitted file)

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(software)

please contact Robert Wax at 703-306-4119 or 703-308-4216,  
for assistance

PSI

Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.